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RAW SEQUENCE LISTING DATE: 01/08/2002
PATENT APPLICATION: US/09/963,340 **TIME:** 10:35:29

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1 <110> APPLICANT: Conkling, Mark
2     Mendum, Nandini
3     Song, Wen
4 <120> TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase
5     Expression
6 <130> FILE REFERENCE: 5051-338
7 <140> CURRENT APPLICATION NUMBER: US/09/963,340
8 <141> CURRENT FILING DATE: 2001-09-24
9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/021,286
W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-10
11 <160> NUMBER OF SEQ ID NOS: 3
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 1399
16 <212> TYPE: DNA
17 <213> ORGANISM: Nicotiana tabacum
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19 <221> NAME/KEY: CDS
20 <222> LOCATION: (52)..(1104)
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23                                         Met Phe
24                                         1
25     aga gct att cct ttc act gct aca gtg cat cct tat gca att aca gct      105
26     Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala
27             5           10           15
28     cca agg ttg gtg gtg aaa atg tca gca ata gcc acc aag aat aca aga      153
29     Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg
30             20          25           30
31     gtg gag tca tta gag gtg aaa cca cca gca cac cca act tat gat tta      201
32     Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu
33             35          40           45           50
34     aag gaa gtt atg aaa ctt gca ctc tct gaa gat gct ggg aat tta gga      249
35     Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly
36             55          60           65
37     gat gtg act tgt aag gcg aca att cct ctt gat atg gaa tcc gat gct      297
38     Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala
39             70          75           80
40     cat ttt cta gca aag gaa gac ggg atc ata gca gga att gca ctt gct      345
41     His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala
42             85          90           95
43     gag atg ata ttc gcg gaa gtt gat cct tca tta aag gtg gag tgg tat      393
44     Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr
45             100         105           110
46     gta aat gat ggc gat aaa gtt cat aaa ggc ttg aaa ttt ggc aaa gta      441
47     Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val
48             115         120           125           130

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49	caa gga aac gct tac aac att gtt ata gct gag agg gtt ctc aat	489
50	Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn	
51	135 140 145	
52	ttt atg caa aga atg agt gga ata gct aca cta act aag gaa atg gca	537
53	Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala	
54	150 155 160	
55	gat gct gca cac cct gct tac atc ttg gag act agg aaa act gct cct	585
56	Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro	
57	165 170 175	
58	gga tta cgt ttg gtg gat aaa tgg gcg gta ttg atc ggt ggg ggg aag	633
59	Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys	
60	180 185 190	
61	aat cac aga atg ggc tta ttt gat atg gta atg ata aaa gac aat cac	681
62	Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His	
63	195 200 205 210	
64	ata tct gct gct gga ggt gtc ggc aaa gct cta aaa tct gtg gat cag	729
65	Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln	
66	215 220 225	
67	tat ttg gag caa aat aaa ctt caa ata ggg gtt gag gtt gaa acc agg	777
68	Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg	
69	230 235 240	
70	aca att gaa gaa gta cgt gag gtt cta gac tat gca tct caa aca aag	825
71	Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys	
72	245 250 255	
73	act tcg ttg act agg ata atg ctg gac aat atg gtt gtt cca tta tct	873
74	Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser	
75	260 265 270	
76	aac gga gat att gat gta tcc atg ctt aag gag gct gta gaa ttg atc	921
77	Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile	
78	275 280 285 290	
79	aat ggg agg ttt gat acg gag gct tca gga aat gtt acc ctt gaa aca	969
80	Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr	
81	295 300 305	
82	gta cac aag att gga caa act ggt gtt acc tac att tct aat ggt gcc	1017
83	Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala	
84	310 315 320	
85	ctg acg cat tcc gtg aaa gca ctt gac att tcc ctg aag atc gat aca	1065
86	Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr	
87	325 330 335	
88	gag ctc gcc ctt gaa gtt gga agg cgt aca aaa cga gca tgagcgccat	1114
89	Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala	
90	340 345 350	
91	tacttctgct atagggttgg agtaaaaagca gctgaatagc tgaaagggtgc aaataagaat	1174
92	cattttacta gttgtcaaac aaaagatcct tcactgtgtatcataaaca aagatgtaaa	1234
93	ttgcgtggaat atctcagatg gctctttcc aaccttattt cttgagttgg taatttcatt	1294
94	atagctttgt tttcatgttt catggaattt gttacaatga aaatacttga tttataagtt	1354
95	tggtgtatgt aaaattctgt gttacttcaa atattttgag atgtt	1399
97	<210> SEQ ID NO: 2	
98	<211> LENGTH: 351	

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99 <212> TYPE: PRT
100 <213> ORGANISM: Nicotiana tabacum
101 <400> SEQUENCE: 2
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104 Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn
105 20 25 30
106 Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr
107 35 40 45
108 Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn
109 50 55 60
110 Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser
111 65 70 75 80
112 Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala
113 85 90 95
114 Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu
115 100 105 110
116 Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly
117 115 120 125
118 Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val
119 130 135 140
120 Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu
121 145 150 155 160
122 Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr
123 165 170 175
124 Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly
125 180 185 190
126 Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp
127 195 200 205
128 Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val
129 210 215 220
130 Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu
131 225 230 235 240
132 Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln
133 245 250 255
134 Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro
135 260 265 270
136 Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu
137 275 280 285
138 Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu
139 290 295 300
140 Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser
141 305 310 315 320
142 Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile
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144 Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
145 340 345 350
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 1053

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149 <212> TYPE: DNA
150 <213> ORGANISM: Nicotiana tabacum
151 <400> SEQUENCE: 3
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154 aaaccaccag cacacccaaac ttatgattta aaggaagtta tgaaacttgc actctctgaa 180
155 gatgctggaa atttaggaga tgtgacttgt aaggcgacaa ttcccttttga tatggaatcc 240
156 gatgctcatt ttcttagcaaa ggaagacggg atcatagcag gaattgcact tgctgagatg 300
157 atattcgcgg aagttgatcc ttcatattaaag gtggagtgtt atgttaaatga tggcgataaaa 360
158 gttcataaaag gcttggaaatt tggcaaaatgta caaggaaacg cttacaacat tgttatagct 420
159 gagagggttgc ttctcaattt tatgcaaaaga atgagtggaa tagctacact aactaaggaa 480
160 atggcagatg ctgcacaccc tgcttacatg ttggagacta ggaaaaactgc tcctggatta 540
161 cggttgtgg ataaaatggc ggttattgatc ggtggggggaa agaatcacag aatgggctta 600
162 tttgatatgg taatgataaa agacaatcac atatctgctg ctggaggtgt cggcaaagct 660
163 ctaaaatctg tggatcagta ttggagcaa aataaacttc aaatagggt tgaggttgaa 720
164 accaggacaa ttgaagaagt acgtgagggtt ctagactatg catctcaaacc aaagacttcg 780
165 ttgacttagga taatgctgga caatatgggtt gttccattat ctaacggaga tattgatgt 840
166 tccatgctta aggaggctgt agaattgatc aatgggaggt ttgatacggg ggcttcagga 900
167 aatgttaccc ttgaaacagt acacaagatt ggacaaaactg gtgttaccta catttctagt 960
168 ggtgccctgaa cgcattccgt gaaagcactt gacattccc tgaagatcga tacagagctc 1020
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VERIFICATION SUMMARY

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